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TECH CENTER 1600/2900

1

SEQUENCE LISTING

<110> Young, Robert

<120> Compounds for Targeting

<130> 43191-256808

<140> US 09/825,012

<141> 2001-04-03

<150> US 60/237,159

<151> 2000-10-02

<150> GB 0008049.9

<151> 2000-04-03

<160> 101

<170> PatentIn version 3.1

<210> 1

<211> 282

<212> PRT

<213> Homo sapiens

<400> 1

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu  
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
35 40 45

A35-

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys

275

280

&lt;210&gt; 2

&lt;211&gt; 1039

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg	180
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ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	300
gtgcagatcc tgagccgcta tgacatcgcc ctgggtccagg aggtcagaga cagccacctg	360
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gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgtcatgttg	720
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gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg	960
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&lt;210&gt; 3

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met  
 1 5 10 15

Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr  
 20 25 30

Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val  
 35 40 45

Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His  
 50 55 60

Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr  
 65 70 75 80

Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr  
 85 90 95

Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu  
 100 105 110

Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe  
 115 120 125

Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile  
 130 135 140

Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu  
 145 150 155 160

Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val  
 165 170 175

Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe  
 180 185 190

Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His  
 195 200 205

Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala  
 210 215 220

Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly  
 225 230 235 240

Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu  
 245 250 255

Val Met Leu Lys  
 260

<210> 4

<211> 783

<212> DNA

<213> Homo sapiens

<400> 4

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agagacagcc acctgactgc cgtggggaag ctgctggaca acctcaatca ggacgcacca	180
gacacctatc actacgtggt cagttagcca ctgggacgga acagctataa ggagcgctac	240
ctgttcgtgt acaggcctga ccagggtgtct gcggtggaca gctactacta cgatgatggc	300
tgcgagccct gcgggaacga caccttcaac cgagagccag ccattgtcag gttcttctcc	360
cgggtcacag aggtcagga gtttgccatt gttcccctgc atgcggcccc gggggacgca	420
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gaggacgtca tggtgatggg cgacttcaat gcgggctgca gctatgtgag accctcccag	540
tggtcatcca tccgcctgtg gacaagcccc accttccagt ggctgatccc cgacagcgct	600
gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtggttgc agggatgctg	660
ctccgagggg ccgttggttc cgactcggtt cttcccttta acttccaggc tgcctatggc	720
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tga	783

<210> 5

<211> 161

<212> PRT

29  
 31783  
 4/10

<213> Homo sapiens

<400> 5

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu  
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
145 150 155 160

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<210> 6

<211> 858

<212> DNA

<213> Homo sapiens

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atgtccaatg ccaccctcgt cagctacatt gtgcagatcc tgagccgcta cgacatcgcc 180  
ctggtccagg aggtcagaga cagccacctg actgccgtgg ggaagctgct ggacaacctc 240  
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tataaggagc gctacctggt cgtgtacagg cctgaccagg tgtctgcggg ggacagctac 360  
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gccccggggg acgcagtagc cgagatcgac gctctctatg acgtctacct ggatgtccaa 540  
gagaaatggg gcttggagga cgtcattgtg atgggcgact tcaatgcggg ctgcagctat 600  
gtgagaccct cccagtggtc atccatccgc ctgtggacaa gcccacctt ccagtggctg 660  
atccccgaca gcgctgacac cacagctaca cccacgcact gtgcctatga caggatcgtg 720  
gttgaggga tgctgctccg aggggcccgtt gttcccgact cggctcttcc ctttaacttc 780  
caggctgcct atggcctgag tgaccaactg gccaagcca tcagtgacca ctatccagtg 840  
gaggtgatgc tgaagtga 858

<210> 7

<211> 721

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

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acctgtaagt ccagtcagag ctttttatat agtagcaatc aaaagatcta cttggcctgg 180  
taccagcaga agccaggtaa ggctccaaag ctgctgatct actgggcatc cactagggaa 240  
tctggtgtgc caagcagatt cagcggtagc ggtagcggta ccgacttcac cttcaccatc 300

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agcagcctcc agccagagga catcgccacc tactactgcc agcaatatta tagatatcct 360
cggacgttcg gccaaaggac caaggtggaa atcaaacgaa ctgtggctgc accatctgtc 420
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 480
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 540
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 600
agcagcaccg tgacgctgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 660
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a 721

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<210> 8

<211> 730

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

<400> 8

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gtgaccatca cctgtaagtc cagtcagagc cttttatata gtagcaatca aaagatctac 180
ttggcctggg accagcagaa gccaggtaag gtcctcaaagc tgctgatcta ctgggcatcc 240
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ttcaccatca gcagcctcca gccagaggac atcgccacct actactgcca gcaatattat 360
agatatcctc ggacgttcgg ccaagggacc aaggtggaaa tcaaacgaac tgtggctgca 420
ccatctgtct tcatcttccc gccatctgat gagcagttga aatctggaac tgcctctgtt 480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaaag tacagtggaa ggtggataac 540
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660
gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720
gagtgttaga 730

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<210> 9

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

<400> 9

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu  
35 40 45

Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys  
50 55 60

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu  
65 70 75 80

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
85 90 95

Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr  
100 105 110

Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gln Gly Thr Lys  
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
                   180                                  185                                  190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
                   195                                  200                                  205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
                   210                                  215                                  220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
   225                                  230                                  235

<210> 10

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 heavy chain

<400> 10

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcttggt ttgcttactg gggccaaggg actctgggtca cagtctcttc agcctccacc	420
aaggggcccat cggtcttccc cctggcaccc tctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc <sup>134</sup> acacatgccc <sup>135</sup> accgtgccc gcacctgaac tctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840

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tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac      900
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cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag     1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa     1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag     1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag     1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgtg gctggactcc     1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg     1320
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<210> 11

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid hinge

<220>

<221> CDS

<222> (1)..(15)

<223>

<400> 11

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Asp Lys Thr His Thr
1          5

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15

<210> 12

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Hybrid hinge

<400> 12

Asp Lys Thr His Thr  
1 5

<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 13

ccgggtaaag ggagcggcgg gctgaagatc gcagccttca ac

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<210> 14

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 14

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42

<210> 15

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 15

Leu	Ser	Leu	Ser	Pro	Gly	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala
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Phe Asn

<210> 16

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 16

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39

<210> 17

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 17

gagagggaca gaggttttcc ctgcgcgcc gacttctag

39

<210> 18

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 18

Leu	Ser	Leu	Ser	Pro	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe
1				5				10					15		

Asn

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 19

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36

<210> 20

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 20

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36

<210> 21

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 21

Leu	Ser	Leu	Ser	Pro	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn
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<210> 22

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 22

gcacctgaag ggagcggcgg gctgaagatc gcagccttca ac 42

<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 23

ggtggcacgg gtcgtggact tccctcgccg cccgacttct ag 42

<210> 24

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 24

Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala  
1 5 10 15

Phe Asn

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 25

gcacctgaag gcgggctgaa gatcgagcc ttcaac

36

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 26

ggtggcacgg gtcgtggact tccgcccagac ttctag

36

<210> 27

<211> 16



<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 27

Pro	Pro	Cys	Pro	Ala	Pro	Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn
1				5					10					15	

<210> 28

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 28

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<210> 29

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 29

ctgttttgag tgtgtacgac acagctcaca ggtggcacag gtcgtggtct cccctcg 57

<210> 30

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 30

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1 5 10 15

Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe  
20 25

<210> 31

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 31

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<210> 32

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 32

ctgttttgag tgtgtacgac acagctcaca ggtggcacag gtcgttgtct cccg 54

<210> 33

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 33

Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
1				5				10						15	

Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe
			20					25

<210> 34

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctgg ttgcttactg gggccaaggg actctgggtc cagtctcctc agcctccacc	420
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggtgtgcc tacagtcttc aggactctac	600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
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gccgttgttc ccgactcggc tcttcccttt aacttccagg ctgcctatgg cctgagtgac 1500
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<210> 35

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 35

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gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
tttgcttggg ttgcttactg gggccaaggg actctgggtca cagtctctc agcctccacc 420
aagggcccat cggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 480

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gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
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tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
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<210> 36

<211> 1563

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 36

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aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc 180

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gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga	360
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gcctccacca agggcccac cgtcttcccc ctggcaccct cctccaagag cacctctggg	480
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gtagccgaga tcgacgtctt ctatgacgtc tacctggatg tccaagagaa atggggcttg	1260
gaggacgtca tgttgatggg cgacttcaat gcgggctgca gctatgtgag accctcccag	1320
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<210> 37

<211> 1554

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1554)

&lt;223&gt;

&lt;400&gt; 37

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
165 170 175	

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggg agc ggc Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly 245 250 255	768
ggg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys 260 265 270	816
atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg 275 280 285	864
tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala 290 295 300	912
gtg ggg aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr 305 310 315 320	960
cac tac gtg gtc agt gag cca ctg gga cgg aac agc tat aag gag cgc His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg 325 330 335	1008
tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac agc tac Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr 340 345 350	1056
tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg 355 360 365	1104
gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc agg gag Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu 370 375 380	1152
ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu 385 390 395 400	1200
atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly 405 410 415	1248



ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat 1296  
 Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr  
                   420                  425                  430

gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc 1344  
 Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr  
                   435                  440                  445

ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg 1392  
 Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr  
                   450                  455                  460

cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg 1440  
 His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly  
                   465                  470                  475                  480

gcc gtt gtt ccc gac tgc gct ctt ccc ttt aac ttc cag gct gcc tat 1488  
 Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr  
                   485                  490                  495

ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg 1536  
 Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
                   500                  505                  510

gag gtg atg ctg aag tga 1554  
 Glu Val Met Leu Lys  
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<210> 38

<211> 517

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 38

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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
                   20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
                   35                  40                  45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50					55					60					
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65					70					75					80
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
				85					90					95	
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
		115					120					125			
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	130					135					140				
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150					155					160
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
			165						170					175	
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
		180						185					190		
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
	195						200					205			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
	210					215					220				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
225					230					235					240
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Gly	Ser	Gly
				245					250					255	
Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	Thr	Lys
			260					265					270		
Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	Ser	Arg
		275					280					285			

Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala  
 290 295 300

Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr  
 305 310 315 320

His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg  
 325 330 335

Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr  
 340 345 350

Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg  
 355 360 365

Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu  
 370 375 380

Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu  
 385 390 395 400

Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly  
 405 410 415

Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr  
 420 425 430

Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr  
 435 440 445

Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr  
 450 455 460

His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly  
 465 470 475 480

Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr  
 485 490 495

Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
 500 505 510

Glu Val Met Leu Lys  
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<210> 39

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 39

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ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat      240
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atcgacgctc tctatgacgt ctacctggat gtccaagaga aatggggctt ggaggacgtc     1260
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gccgttggtc ccgactcggc ttttcccttt aacttccagg ctgcctatgg cctgagtgc 1500
caactggccc aagccatcag tgaccactat ccagtggagg tgatgctgaa ggggggcgga 1560
cccaaaaaga agcgcaaggt ttga 1584

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<210> 40

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 40

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 atccgcctgt ggacaagccc caccttccag tggctgatcc ccgacagcgc tgacaccaca 1380  
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 gccgttgttc ccgactcggc tcttcccttt aacttccagg ctgcctatgg cctgagtgac 1500  
 caactggccc aagccatcag tgaccactat ccagtggagg tgatgctgaa ggggggcgga 1560  
 cccaaaaaga agcgcaaggt ttga 1584

<210> 41

<211> 1593

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 41

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 cactcccagg tgcagctggt gcagtctggg gcagaggtga aaaagcctgg ggcctcagtg 120  
 aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc 180  
 caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct 240  
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 gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga 360  
 tcctacgact ttgcctggtt tgcttactgg ggccaaggga ctctggtcac agtctcctca 420  
 gcctccacca agggcccac cgtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 540  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660

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tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aaatcttgtg acaaaaactca cacatgtcca ccgtgtccag caccagaggg gagcggcggg 780
ctgaagatcg cagccttcaa catccagaca tttggggaga ccaagatgtc caatgccacc 840
ctcgtcagct acattgtgca gatcctgagc cgctacgaca tcgccctggt ccaggagggtc 900
agagacagcc acctgactgc cgtggggaag ctgctggaca acctcaatca ggacgcacca 960
gacacctatc actacgtggt cagtgaagcca ctgggacgga acagctataa ggagcgctac 1020
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tgcgagccct gcgggaacga caccttcaac cgagagccag ccattgtcag gttcttctcc 1140
cggttcacag aggtcaggga gtttgccatt gttcccctgc atgcggcccc gggggacgca 1200
gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaagagaa atggggcttg 1260
gaggacgtca tgttgatggg cgacttcaat gcgggctgca gctatgtgag accctcccag 1320
tggtcatcca tccgcctgtg gacaagcccc accttccagt ggctgatccc cgacagcgct 1380
gacaccacag ctacaccac gcactgtgcc tatgacagga tcgtgggttg agggatgctg 1440
ctccgagggg ccgttggttc cgactcggct cttcccttta acttccaggc tgccatggc 1500
ctgagtgacc aactggccca agccatcagt gaccactatc cagtggaggt gatgctgaag 1560
gggggcggac caaaaaagaa gcgcaagggt tga 1593

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<210> 42

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1584)

<223>

<400> 42

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
165 170 175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
180 185 190	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	
195 200 205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac	672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	
210 215 220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt	720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys	
225 230 235 240	



gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ggg	agc	ggc	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Gly	Ser	Gly	
				245					250					255		
ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	ggg	gag	acc	aag	816
Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	Thr	Lys	
			260					265					270			
atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	atc	ctg	agc	cgc	864
Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	Ser	Arg	
		275						280				285				
tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	cac	ctg	act	gcc	912
Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	Thr	Ala	
	290					295					300					
gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	cca	gac	acc	tat	960
Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	Thr	Tyr	
305					310					315					320	
cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	tat	aag	gag	cgc	1008
His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	Glu	Arg	
				325					330					335		
tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac	agc	tac	1056
Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	Ser	Tyr	
			340					345					350			
tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	ttc	aac	cga	1104
Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	Asn	Arg	
		355					360					365				
gag	cca	gcc	att	gtc	agg	ttc	ttc	tcc	cgg	ttc	aca	gag	gtc	agg	gag	1152
Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	Glu	Val	Arg	Glu	
	370					375					380					
ttt	gcc	att	gtt	ccc	ctg	cat	gcg	gcc	ccg	ggg	gac	gca	gta	gcc	gag	1200
Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val	Ala	Glu	
385					390					395					400	
atc	gac	gct	ctc	tat	gac	gtc	tac	ctg	gat	gtc	caa	gag	aaa	tgg	ggc	1248
Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys	Trp	Gly	
				405					410					415		
ttg	gag	gac	gtc	atg	ttg	atg	ggc	gac	ttc	aat	gcg	ggc	tgc	agc	tat	1296
Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	Gly	Cys	Ser	Tyr	
			420					425					430			
gtg	aga	ccc	tcc	cag	tgg	tca	tcc	atc	cgc	ctg	tgg	aca	agc	ccc	acc	1344
Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	Thr	Ser	Pro	Thr	
		435					440					445				
ttc	cag	tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	aca	gct	aca	ccc	acg	1392
Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr	Pro	Thr	
	450					455					460					
cac	tgt	gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	atg	ctg	ctc	cga	ggg	1440
His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	Leu	Leu	Arg	Gly	

465				470				475				480				
gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	aac	ttc	cag	gct	gcc	tat	1488
Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn	Phe	Gln	Ala	Ala	Tyr	
				485					490					495		
ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac	cac	tat	cca	gtg	1536
Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp	His	Tyr	Pro	Val	
				500					505					510		
gag	gtg	atg	ctg	aag	ggg	ggc	gga	ccc	aaa	aag	aag	cgc	aag	gtt	tga	1584
Glu	Val	Met	Leu	Lys	Gly	Gly	Gly	Pro	Lys	Lys	Lys	Arg	Lys	Val		
				515					520					525		

<210> 43

<211> 527

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 43

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125  
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140  
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160  
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175  
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190  
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205  
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220  
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly  
 245 250 255  
 Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys  
 260 265 270  
 Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg  
 275 280 285  
 Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala  
 290 295 300  
 Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr  
 305 310 315 320  
 His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg  
 325 330 335  
 Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr  
 340 345 350

Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg  
           355                                  360                                  365

Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu  
           370                                  375                                  380

Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu  
   385                                  390                                  395                                  400

Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly  
                                   405                                  410                                  415

Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr  
                                   420                                  425                                  430

Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr  
                                   435                                  440                                  445

Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr  
           450                                  455                                  460

His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly  
   465                                  470                                  475                                  480

Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr  
                                   485                                  490                                  495

Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
                                   500                                  505                                  510

Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys Val  
           515                                  520                                  525

<210> 44

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 44  
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180  
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240  
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
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gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540  
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tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 660  
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720  
gacaaaactc acacatgccc accgtgccc gcacctgaac tcctgggggg accgtcagtc 780  
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gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1140  
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200  
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1260  
gacggctcct tcttctctca cagcaagctc accgtggaca agagcaggtg gcagcagggg 1320  
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agccgctacg acatcgccct ggtccaggag gtcagagaca gccacctgac tgccgtgggg 1560  
aagctgctgg acaacctcaa tcaggacgca ccagacacct atcactacgt ggtcagttag 1620  
ccactgggac ggaacagcta taaggagcgc tacctgttcg tgtacaggcc tgaccaggtg 1680  
tctgcggtgg acagctacta ctacgatgat ggctgcgagc cctgcgggaa cgacaccttc 1740

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aaccgagagc cagccattgt caggtttcttc tcccggttca cagaggtcag ggagtttgcc 1800
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gtctacctgg atgtccaaga gaaatggggc ttggaggacg tcatgttgat gggcgacttc 1920
aatgcgggct gcagctatgt gagaccctcc cagtggtcac ccatccgcct gtggacaagc 1980
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<210> 45

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2196)

<223>

<400> 45

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
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1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240

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Glu 65	Trp	Val	Gly	Glu	Ile 70	Leu	Pro	Gly	Ser	Asn 75	Asn	Ser	Arg	Tyr	Asn 80	
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Glu	Lys	Phe	Lys	Gly 85	Arg	Val	Thr	Val	Thr 90	Arg	Asp	Thr	Ser	Thr	Asn 95	
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met 100	Glu	Leu	Ser	Ser	Leu 105	Arg	Ser	Glu	Asp	Thr	Ala	Val	
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys 115	Ala	Arg	Ser	Tyr	Asp 120	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly 130	Thr	Leu	Val	Thr	Val 135	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro 150	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala 160	
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Ala	Leu	Gly	Cys 165	Leu	Val	Lys	Asp	Tyr	Phe 170	Pro	Glu	Pro	Val	Thr	Val	
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Ser	Trp	Asn 180	Ser	Gly	Ala	Leu	Thr	Ser 185	Gly	Val	His	Thr	Phe	Pro	Ala	
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Val	Leu 195	Gln	Ser	Ser	Gly	Leu	Tyr 200	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser 210	Ser	Ser	Leu	Gly	Thr 215	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys 230	Val	Asp	Lys	Lys 235	Val	Glu	Pro	Lys	Ser	Cys 240	
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Asp	Lys	Thr	His 245	Thr	Cys	Pro	Pro	Cys	Pro 250	Ala	Pro	Glu	Leu	Leu	Gly	
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val 260	Phe	Leu	Phe	Pro 265	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg 275	Thr	Pro	Glu	Val	Thr 280	Cys	Val	Val	Val	Asp	Val	Ser	His	
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp 290	Pro	Glu	Val	Lys	Phe 295	Asn	Trp	Tyr	Val	Asp 300	Gly	Val	Glu	Val	

cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
305					310					315					320	
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				325					330					335		
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
			340					345					350			
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		355					360					365				
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
	370					375					380					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
385					390					395					400	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
			405					410						415		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
			420					425					430			
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	1344
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
		435					440					445				
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	1392
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
	450					455					460					
ccg	ggt	aaa	ggg	agc	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	1440
Pro	Gly	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	
465					470					475					480	
aca	ttt	ggg	gag	acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	1488
Thr	Phe	Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	
			485					490						495		
gtg	cag	atc	ctg	agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	1536
Val	Gln	Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	
			500					505					510			
gac	agc	cac	ctg	act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	1584
Asp	Ser	His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	
		515					520					525				
gac	gca	cca	gac	acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	1632
Asp	Ala	Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	
	530					535					540					



aac agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg	1680
Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val	
545 550 555 560	
tct gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg	1728
Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly	
565 570 575	
aac gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg	1776
Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg	
580 585 590	
ttc aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg	1824
Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro	
595 600 605	
ggg gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat	1872
Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp	
610 615 620	
gtc caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc	1920
Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe	
625 630 635 640	
aat gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc	1968
Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg	
645 650 655	
ctg tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac	2016
Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp	
660 665 670	
acc aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca	2064
Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala	
675 680 685	
ggg atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt	2112
Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe	
690 695 700	
aac ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc	2160
Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile	
705 710 715 720	
agt gac cac tat cca gtg gag gtg atg ctg aag tga	2196
Ser Asp His Tyr Pro Val Glu Val Met Leu Lys	
725 730	

&lt;210&gt; 46

&lt;211&gt; 731

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 46

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln  
 465 470 475 480

Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile  
 485 490 495

Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg  
 500 505 510

Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln  
 515 520 525

Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg  
 530 535 540

Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val  
 545 550 555 560

Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly  
 565 570 575

Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg  
 580 585 590

Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro  
 595 600 605

Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp  
 610 615 620

Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe  
 625 630 635 640

Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg  
 645 650 655

Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp  
 660 665 670

Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala

675		680		685
Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe				
690		695		700
Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile				
705		710		715
				720
Ser Asp His Tyr Pro Val Glu Val Met Leu Lys				
		725		730

&lt;210&gt; 47

&lt;211&gt; 2193

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 47

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccag	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tgcagtgggt cggagagatt ttacctgga gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctgg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctocacc	420
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcttc aggactctac	600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatottgt	720
gacaaaactc acacatgccc accgtgccc gacactgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900

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ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 960
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccg tctggactcc 1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380
ctctccctgt ctccgaaggg gagcggcggg ctgaagatcg cagccttcaa catccagaca 1440
tttggggaga ccaagatgtc caatgccacc ctcgtcagct acattgtgca gatcctgagc 1500
cgctacgaca tcgccctggt ccaggagggtc agagacagcc acctgactgc cgtggggaag 1560
ctgctggaca acctcaatca ggacgcacca gacacctatc actacgtggt cagtgaacca 1620
ctgggacgga acagctataa ggagcgctac ctgttcgtgt acaggcctga ccagggtgtct 1680
gcggtggaca gctactacta cgatgatggc tgcgagccct gcgggaacga caccttcaac 1740
cgagagccag ccattgtcag gttcttctcc cggttcacag aggtcaggga gtttgccatt 1800
gttcccctgc atgcggcccc gggggacgca gtagccgaga tcgacgctct ctatgacgtc 1860
tacctggatg tccaagagaa atggggcttg gaggacgtca tgttgatggg cgacttcaat 1920
gcggggtgca gctatgtgag accctcccag tggatcatcca tccgcctgtg gacaagcccc 1980
accttccagt ggctgatccc cgacagcgct gacaccacag ctacaccac gactgtgcc 2040
tatgacagga tcgtggttgc agggatgctg ctccgagggg ccgttgttcc cgactcggct 2100
cttcccttta acttccaggc tgcctatggc ctgagtgacc aactggccca agccatcagt 2160
gaccactatc cagtggaggt gatgctgaag tga 2193

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<210> 48

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (2193)

&lt;223&gt;

&lt;400&gt; 48

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
165 170 175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
180 185 190	

gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
				245					250					255		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260					265					270			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		275					280					285				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	290					295					300					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
305					310					315					320	
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				325					330					335		
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
			340					345					350			
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		355					360					365				
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
		370				375					380					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
385				390						395					400	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
				405				410						415		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	



420					425					430							
gac Asp	aag Lys	agc Ser 435	agg Arg	tgg Trp	cag Gln	cag Gln	ggg Gly 440	aac Asn	gtc Val	ttc Phe	tca Ser	tgc Cys 445	tcc Ser	gtg Val	atg Met	1344	
cat His	gag Glu 450	gct Ala	ctg Leu	cac His	aac Asn	cac His 455	tac Tyr	acg Thr	cag Gln	aag Lys	agc Ser 460	ctc Leu	tcc Ser	ctg Leu	tct Ser	1392	
ccg Pro 465	aag Lys	ggg Gly	agc Ser	ggc Gly	ggg Gly 470	ctg Leu	aag Lys	atc Ile	gca Ala	gcc Ala 475	ttc Phe	aac Asn	atc Ile	cag Gln	aca Thr 480	1440	
ttt Phe	ggg Gly	gag Glu	acc Thr	aag Lys 485	atg Met	tcc Ser	aat Asn	gcc Ala 490	acc Thr	ctc Leu	gtc Val	agc Ser	tac Tyr	att Ile 495	gtg Val	1488	
cag Gln	atc Ile	ctg Leu	agc Ser 500	cgc Arg	tac Tyr	gac Asp	atc Ile	gcc Ala 505	ctg Leu	gtc Val	cag Gln	gag Glu	gtc Val 510	aga Arg	gac Asp	1536	
agc Ser	cac His	ctg Leu 515	act Thr	gcc Ala	gtg Val	ggg Gly 520	aag Lys	ctg Leu	ctg Leu	gac Asp	aac Asn	ctc Leu 525	aat Asn	cag Gln	gac Asp	1584	
gca Ala	cca Pro 530	gac Asp	acc Thr	tat Tyr	cac His	tac Tyr 535	gtg Val	gtc Val	agt Ser	gag Glu	cca Pro 540	ctg Leu	gga Gly	cgg Arg	aac Asn	1632	
agc Ser 545	tat Tyr	aag Lys	gag Glu	cgc Arg	tac Tyr 550	ctg Leu	ttc Phe	gtg Val	tac Tyr	agg Arg 555	cct Pro	gac Asp	cag Gln	gtg Val	tct Ser 560	1680	
gcg Ala	gtg Val	gac Asp	agc Ser 565	tac Tyr	tac Tyr	tac Tyr	gat Asp	gat Asp	ggc Gly 570	tgc Cys	gag Glu	ccc Pro	tgc Cys	ggg Gly 575	aac Asn	1728	
gac Asp	acc Thr	ttc Phe	aac Asn 580	cga Arg	gag Glu	cca Pro	gcc Ala	att Ile 585	gtc Val	agg Arg	ttc Phe	ttc Phe	tcc Ser 590	cgg Arg	ttc Phe	1776	
aca Thr	gag Glu	gtc Val 595	agg Arg	gag Glu	ttt Phe	gcc Ala	att Ile 600	gtt Val	ccc Pro	ctg Leu	cat His	gcg Ala 605	gcc Ala	ccg Pro	ggg Gly	1824	
gac Asp	gca Ala 610	gta Val	gcc Ala	gag Glu	atc Ile	gac Asp 615	gct Ala	ctc Leu	tat Tyr	gac Asp	gtc Val 620	tac Tyr	ctg Leu	gat Asp	gtc Val	1872	
caa Gln 625	gag Glu	aaa Lys	tgg Trp	ggc Gly	ttg Leu 630	gag Glu	gac Asp	gtc Val	atg Met	ttg Leu 635	atg Met	ggc Gly	gac Asp	ttc Phe	aat Asn 640	1920	
gcg Ala	ggc Gly	tgc Cys	agc Ser	tat Tyr 645	gtg Val	aga Arg	ccc Pro	tcc Ser	cag Gln 650	tgg Trp	tca Ser	tcc Ser	atc Ile	cgc Arg 655	ctg Leu	1968	
tgg	aca	agc	ccc	acc	ttc	cag	tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	2016	

Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr		
			660					665					670				
aca	gct	aca	ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	2064	
Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly		
			675				680					685					
atg	ctg	ctc	cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	aac	2112	
Met	Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn		
	690					695					700						
ttc	cag	gct	gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	2160	
Phe	Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser		
705					710					715					720		
gac	cac	tat	cca	gtg	gag	gtg	atg	ctg	aag	tga						2193	
Asp	His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys								
				725					730								

&lt;210&gt; 49

&lt;211&gt; 730

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 49

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
	50					55					60				

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65					70					75					80

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
				85					90					95	

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
 465 470 475 480

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
 485 490 495

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
 500 505 510

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
 515 520 525

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
 530 535 540

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
 545 550 555 560

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn

				565				570				575			
Asp	Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe
580								585				590			
Thr	Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly
595								600				605			
Asp	Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val
610								615				620			
Gln	Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn
625								630				635			
Ala	Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu
				645								655			
Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr
				660				665				670			
Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly
675								680				685			
Met	Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn
690								695				700			
Phe	Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser
705								710				715			
Asp	His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys						
				725				730							

<210> 50

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 50

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gtgcagctgg	tgcagtctgg	ggcagaggtg	aaaaagcctg	gggcctcagt	gaaggtgtcc	120
tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagatacaat	240
gagaagttca	agggccgagt	gacagtcact	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgccctgg	ttgcttactg	gggccaaagg	actctgggtc	cagtctcctc	agcctccacc	420
aagggcccat	cggctcttcc	cctggcacc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacgggtgc	gtggaactca	540
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcttc	aggactctac	600
tcctcagca	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcaccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaactctgt	720
gacaaaactc	acacatgccc	accgtgcca	gcacctgaac	tcctgggggg	accgtcagtc	780
ttcctcttcc	ccccaaaacc	caaggacacc	ctcatgatct	cccgacccc	tgaggtcaca	840
tgcggtgggtg	tggtggtgag	ccacgaagac	cctgaggtca	agttcaactg	gtacgtggac	900
ggcggtggagg	tgcataatgc	caagacaaag	ccgcggggagg	agcagtacaa	cagcacgtac	960
cgtgtggtca	gcgtcctcac	cgtcctgcac	caggactggc	tgaatggcaa	ggagtacaag	1020
tgcaaggctt	ccaacaaagc	cctcccagcc	cccatcgaga	aaaccatctc	caaagccaaa	1080
gggcagcccc	gagaaccaca	ggtgtacacc	ctgcccccat	cccgggatga	gctgaccaag	1140
aaccaggtca	gcctgacctg	cctgggtcaaa	ggcttctatc	ccagcgacat	cgccgtggag	1200
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgcctcccgt	gctggactcc	1260
gacggctcct	tcttctctta	cagcaagctc	accgtggaca	agagcaggtg	gcagcagggg	1320
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	1380
ctctccctgt	ccccggggag	cggcggggtg	aagatcgag	ccttcaacat	ccagacattt	1440
ggggagacca	agatgtccaa	tgccaccctc	gtcagctaca	ttgtgcagat	cctgagccgc	1500
tacgacatcg	ccctgggtcca	ggaggtcaga	gacagccacc	tgactgccgt	ggggaagctg	1560
ctggacaacc	tcaatcagga	cgcaccagac	acctatcact	acgtgggtcag	tgagccactg	1620
ggacggaaca	gctataagga	gcgtacctg	ttcgtgtaca	ggcctgacca	ggtgtctgcg	1680
gtggacagct	actactacga	tgatgggtgc	gagccctgcg	ggaacgacac	cttcaaccga	1740
gagccagcca	ttgtcaggtt	cttctcccgg	ttcacagagg	tcaggaggtt	tgccattgtt	1800

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ccccgcatg cggccccggg ggacgcagta gccgagatcg acgctctcta tgacgtctac 1860
ctggatgtcc aagagaaatg gggcttggag gacgtcatgt tgatgggcga cttcaatgcg 1920
ggctgcagct atgtgagacc ctcccagtgg tcatccatcc gcctgtggac aagccccacc 1980
ttccagtggc tgatccccga cagcgctgac accacagcta caccacgca ctgtgcctat 2040
gacaggatcg tggttgcagg gatgctgctc cgaggggccg ttgttcccga ctcggtcttt 2100
ccctttaact tccaggctgc ctatggcctg agtgaccaac tggcccaagc catcagtgac 2160
cactatccag tggaggtgat gctgaagtga 2190

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<210> 51

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2190)

<223>

<400> 51

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

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gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
165 170 175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
180 185 190	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	
195 200 205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac	672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	
210 215 220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt	720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys	
225 230 235 240	
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg	768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly	
245 250 255	
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg	816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met	
260 265 270	
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac	864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His	
275 280 285	
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg	912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val	
290 295 300	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac	960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	



305					310					315					320		
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc		1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly		
				325					330					335			
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc		1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile		
			340					345					350				
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg		1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val		
		355					360					365					
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc		1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser		
	370					375					380						
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag		1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu		
385					390					395					400		
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc		1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro		
			405					410						415			
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg		1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val		
			420				425						430				
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg		1344
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met		
		435					440					445					
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tcc		1392
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser		
	450				455						460						
ccg	ggg	agc	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt		1440
Pro	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe		
465					470					475					480		
ggg	gag	acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag		1488
Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln		
				485					490					495			
atc	ctg	agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc		1536
Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser		
			500					505					510				
cac	ctg	act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca		1584
His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala		
		515					520					525					
cca	gac	acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc		1632
Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser		
	530					535					540						
tat	aag	gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg		1680

Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala		
545					550					555					560		
gtg	gac	agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac		1728
Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp		
				565				570						575			
acc	ttc	aac	cga	gag	cca	gcc	att	gtc	agg	ttc	ttc	tcc	cgg	ttc	aca		1776
Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr		
			580					585					590				
gag	gtc	agg	gag	ttt	gcc	att	gtt	ccc	ctg	cat	gcg	gcc	ccg	ggg	gac		1824
Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp		
		595					600					605					
gca	gta	gcc	gag	atc	gac	gct	ctc	tat	gac	gtc	tac	ctg	gat	gtc	caa		1872
Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln		
	610					615					620						
gag	aaa	tgg	ggc	ttg	gag	gac	gtc	atg	ttg	atg	ggc	gac	ttc	aat	gcg		1920
Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala		
625					630			635							640		
ggc	tgc	agc	tat	gtg	aga	ccc	tcc	cag	tgg	tca	tcc	atc	cgc	ctg	tgg		1968
Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp		
				645				650						655			
aca	agc	ccc	acc	ttc	cag	tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	aca		2016
Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr		
			660					665					670				
gct	aca	ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	atg		2064
Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met		
		675					680					685					
ctg	ctc	cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	aac	ttc		2112
Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn	Phe		
	690					695					700						
cag	gct	gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac		2160
Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp		
705					710				715						720		
cac	tat	cca	gtg	gag	gtg	atg	ctg	aag	tga								2190
His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys									
				725													

&lt;210&gt; 52

&lt;211&gt; 729

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 52

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His

210					215					220					
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
225					230					235					240
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
				245					250					255	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			260					265					270		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
		275					280					285			
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	290					295					300				
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
305					310					315					320
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
				325					330					335	
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
			340					345					350		
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
		355					360					365			
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
	370					375					380				
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
385					390					395					400
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
			405						410					415	
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
			420					425					430		
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
		435					440					445			

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 465 470 475 480

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 485 490 495

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 500 505 510

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 515 520 525

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 530 535 540

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 545 550 555 560

Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 565 570 575

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 580 585 590

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 595 600 605

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
 610 615 620

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
 625 630 635 640

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
 645 650 655

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
 660 665 670

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
 675 680 685

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
 690 695 700

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
 705 710 715 720

His Tyr Pro Val Glu Val Met Leu Lys  
 725

<210> 53

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 53

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctgg ttgcttactg gggccaaggg actctgggtca cagtctctc agcctccacc	420
aagggcccat cggctctccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggtgtgtc tacagtctc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgocca gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960

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cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1140
aaccagggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1260
gacggctcct tcttctctta cagcaagctc accgtggaca agagcagggtg gcagcagggg 1320
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ctctccctgt ctccgggtaa agggagcggc gggctgaaga tcgcagcctt caacatccag 1440
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agccgctacg acatcgccct ggtccaggag gtcagagaca gccacctgac tgccgtgggg 1560
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ccactgggac ggaacagcta taaggagcgc tacctgttcg tgtacaggcc tgaccagggtg 1680
tctgcggtgg acagctacta ctacgatgat ggctgcgagc cctgcgggaa cgacaccttc 1740
aaccgagagc cagccattgt caggttcttc tcccggttca cagaggtcag ggagtttgcc 1800
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gtctacctgg atgtccaaga gaaatggggc ttggaggacg tcatgttgat gggcgacttc 1920
aatgcgggct gcagctatgt gagaccctcc cagtggcat ccatccgcct gtggacaagc 1980
cccaccttcc agtggctgat ccccgacagc gctgacacca cagctacacc cagcactgt 2040
gcctatgaca ggatcgtggt tgcagggatg ctgctccgag gggccgttgt tcccgactcg 2100
gctcttccct ttaacttcca ggctgcctat ggctgagtg accaactggc ccaagccatc 2160
agtgaccact atccagtgga ggtgatgctg aaggggggcg gacccaaaaa gaagcgcaag 2220
gtttga 2226

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<210> 54

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2226)

&lt;223&gt;

&lt;400&gt; 54

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
165 170 175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
180 185 190	



gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
				245					250					255		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260					265					270			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	864
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
		275					280					285				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	912
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
	290					295					300					
cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	960
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
305					310					315					320	
cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	1008
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
				325					330					335		
aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	1056
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	
			340					345					350			
gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	1104
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
		355					360					365				
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	1152
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
		370				375					380					
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	1200
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
385				390						395					400	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	1248
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
			405					410						415		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	

420					425					430						
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	1344
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
		435					440					445				
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	1392
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
	450					455					460					
ccg	ggt	aaa	ggg	agc	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	1440
Pro	Gly	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	
465					470					475					480	
aca	ttt	ggg	gag	acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	1488
Thr	Phe	Gly	Glu	Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	
				485					490					495		
gtg	cag	atc	ctg	agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	1536
Val	Gln	Ile	Leu	Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	
			500					505					510			
gac	agc	cac	ctg	act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	1584
Asp	Ser	His	Leu	Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	
		515					520					525				
gac	gca	cca	gac	acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	1632
Asp	Ala	Pro	Asp	Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	
	530					535					540					
aac	agc	tat	aag	gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	1680
Asn	Ser	Tyr	Lys	Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	
545					550					555					560	
tct	gcg	gtg	gac	agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	1728
Ser	Ala	Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	
				565					570					575		
aac	gac	acc	ttc	aac	cga	gag	cca	gcc	att	gtc	agg	ttc	ttc	tcc	cgg	1776
Asn	Asp	Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	
			580					585					590			
ttc	aca	gag	gtc	agg	gag	ttt	gcc	att	gtt	ccc	ctg	cat	gcg	gcc	ccg	1824
Phe	Thr	Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	
		595					600					605				
ggg	gac	gca	gta	gcc	gag	atc	gac	gct	ctc	tat	gac	gtc	tac	ctg	gat	1872
Gly	Asp	Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	
	610					615					620					
gtc	caa	gag	aaa	tgg	ggc	ttg	gag	gac	gtc	atg	ttg	atg	ggc	gac	ttc	1920
Val	Gln	Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	
625					630					635					640	
aat	gcg	ggc	tgc	agc	tat	gtg	aga	ccc	tcc	cag	tgg	tca	tcc	atc	cgc	1968
Asn	Ala	Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	
				645					650					655		
ctg	tgg	aca	agc	ccc	acc	ttc	cag	tgg	ctg	atc	ccc	gac	agc	gct	gac	2016

Leu	Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	
			660					665						670		
acc	aca	gct	aca	ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	gtt	gca	2064
Thr	Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	
			675				680					685				
ggg	atg	ctg	ctc	cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	2112
Gly	Met	Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	
	690					695					700					
aac	ttc	cag	gct	gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	2160
Asn	Phe	Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	
705					710					715					720	
agt	gac	cac	tat	cca	gtg	gag	gtg	atg	ctg	aag	ggg	ggc	gga	ccc	aaa	2208
Ser	Asp	His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys	Gly	Gly	Gly	Pro	Lys	
				725					730					735		
aag	aag	cgc	aag	ggt	tga											2226
Lys	Lys	Arg	Lys	Val												
			740													

&lt;210&gt; 55

&lt;211&gt; 741

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 55

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
	50					55					60				
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65					70					75					80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430  
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445  
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460  
 Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln  
 465 470 475 480  
 Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile  
 485 490 495  
 Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg  
 500 505 510  
 Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln  
 515 520 525  
 Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg  
 530 535 540  
 Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val

545		550		555		560									
Ser	Ala	Val	Asp	Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly
				565					570					575	
Asn	Asp	Thr	Phe	Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg
			580					585						590	
Phe	Thr	Glu	Val	Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro
		595					600					605			
Gly	Asp	Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp
	610					615					620				
Val	Gln	Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe
625					630					635					640
Asn	Ala	Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg
				645					650					655	
Leu	Trp	Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp
			660					665					670		
Thr	Thr	Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala
		675					680					685			
Gly	Met	Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe
	690					695					700				
Asn	Phe	Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile
705					710					715					720
Ser	Asp	His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys	Gly	Gly	Gly	Pro	Lys
				725					730					735	
Lys	Lys	Arg	Lys	Val											
			740												

&lt;210&gt; 56

&lt;211&gt; 2223

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 56

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gtgcagctgg tgcagtctgg ggcagagggtg aaaaagcctg gggcctcagt gaagggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctgg ttgcttactg gggccaagggt actctgggtc cagtctcttc agcctccacc	420
aaggggcccat cggctcttccc cctggcacccc tcctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcttc aggactctac	600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgcca gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtgggtg tggacgtgag ccacgaagac cctgagggtc agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtgggtc gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaagggtc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	1080
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag	1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag	1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc	1260
gacggctcct tcttctctca cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ctccgaaggg gagcggcggg ctgaagatcg cagccttcaa catccagaca	1440
tttggggaga ccaagatgtc caatgccacc ctcgtcagct acattgtgca gatcctgagc	1500
cgctacgaca tcgccctggg ccaggagggtc agagacagcc acctgactgc cgtggggaag	1560

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ctgctggaca acctcaatca ggacgcacca gacacctatc actacgtggt cagtgaacca 1620
ctgggacgga acagctataa ggagcgctac ctgttcgtgt acaggcctga ccagggtgtct 1680
gcggtggaca gctactacta cgatgatggc tgcgagccct gcgggaacga caccttcaac 1740
cgagagccag ccattgtcag gttcttctcc cggttcacag aggtcaggga gtttgccatt 1800
gttcccctgc atgcggcccc gggggacgca gtagccgaga tcgacgctct ctatgacgtc 1860
tacctggatg tccaagagaa atggggcttg gaggacgtca tggtgatggg cgacttcaat 1920
gcgggctgca gctatgtgag accctcccag tggatcatcca tccgcctgtg gacaagcccc 1980
accttcaggt ggctgatccc cgacagcgct gacaccacag ctacaccac gcactgtgcc 2040
tatgacagga tcgtgggttg agggatgctg ctccgagggg ccgttggttc cgactcggct 2100
cttcccttta acttcaggc tgcctatggc ctgagtgacc aactggccca agccatcagt 2160
gaccactatc cagtggaggt gatgctgaag gggggcggac caaaaagaa gcgcaaggtt 2220
tga 2223

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<210> 57

<211> 2223

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2223)

<223>

<400> 57

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144

```



Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
	35						40					45				
agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55				60						
gag	tgg	gtc	gga	gag	att	tta	cct	gga	agt	aat	aat	tct	aga	tac	aat	240
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70					75					80	
gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
				85					90					95		
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	768
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
				245					250					255		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	816
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			260				265						270			

atc Ile	tcc Ser	cgg Arg 275	acc Thr	cct Pro	gag Glu	gtc Val	aca Thr 280	tgc Cys	gtg Val	gtg Val	gtg Val	gac Asp 285	gtg Val	agc Ser	cac His	864
gaa Glu	gac Asp 290	cct Pro	gag Glu	gtc Val	aag Lys	ttc Phe 295	aac Asn	tgg Trp	tac Tyr	gtg Val	gac Asp 300	ggc Gly	gtg Val	gag Glu	gtg Val	912
cat His 305	aat Asn	gcc Ala	aag Lys	aca Thr 310	aag Lys	ccg Pro	cgg Arg	gag Glu	gag Glu	cag Gln 315	tac Tyr	aac Asn	agc Ser	acg Thr 320	tac Tyr	960
cgt Arg	gtg Val	gtc Val	agc Ser 325	gtc Val	ctc Leu	acc Thr	gtc Val	ctg Leu	cac His 330	cag Gln	gac Asp	tgg Trp	ctg Leu	aat Asn 335	ggc Gly	1008
aag Lys	gag Glu	tac Tyr 340	aag Lys	tgc Cys	aag Lys	gtc Val	tcc Ser 345	aac Asn	aaa Lys	gcc Ala	ctc Leu	cca Pro	gcc Ala 350	ccc Pro	atc Ile	1056
gag Glu	aaa Lys 355	acc Thr	atc Ile	tcc Ser	aaa Lys	gcc Ala	aaa Lys 360	ggg Gly	cag Gln	ccc Pro	cga Arg	gaa Glu 365	cca Pro	cag Gln	gtg Val	1104
tac Tyr	acc Thr 370	ctg Leu	ccc Pro	cca Pro	tcc Ser	cgg Arg 375	gat Asp	gag Glu	ctg Leu	acc Thr 380	aag Lys	aac Asn	cag Gln	gtc Val	agc Ser	1152
ctg Leu 385	acc Thr	tgc Cys	ctg Leu	gtc Val	aaa Lys 390	ggc Gly	ttc Phe	tat Tyr	ccc Pro	agc Ser 395	gac Asp	atc Ile	gcc Ala	gtg Val	gag Glu 400	1200
tgg Trp	gag Glu	agc Ser	aat Asn 405	ggg Gly 410	cag Gln	ccg Pro	gag Glu	aac Asn	aac Asn	tac Tyr 415	aag Lys	acc Thr	acg Thr	cct Pro 420	ccc Pro	1248
gtg Val	ctg Leu	gac Asp 420	tcc Ser	gac Asp	ggc Gly	tcc Ser	ttc Phe 425	ttc Phe	ctc Leu	tac Tyr	agc Ser	aag Lys 430	ctc Leu	acc Thr	gtg Val	1296
gac Asp	aag Lys 435	agc Ser	agg Arg	tgg Trp	cag Gln	cag Gln	ggg Gly 440	aac Asn	gtc Val	ttc Phe	tca Ser	tgc Cys 445	tcc Ser	gtg Val	atg Met	1344
cat His 450	gag Glu	gct Ala	ctg Leu	cac His	aac Asn	cac His 455	tac Tyr	acg Thr	cag Gln	aag Lys	agc Ser 460	ctc Leu	tcc Ser	ctg Leu	tct Ser	1392
ccg Pro 465	aag Lys	ggg Gly	agc Ser	ggc Gly	ggg Gly 470	ctg Leu	aag Lys	atc Ile	gca Ala	gcc Ala 475	ttc Phe	aac Asn	atc Ile	cag Gln	aca Thr 480	1440
ttt Phe	ggg Gly	gag Glu	acc Thr 485	aag Lys	atg Met	tcc Ser	aat Asn	gcc Ala	acc Thr 490	ctc Leu	gtc Val	agc Ser	tac Tyr	att Ile 495	gtg Val	1488
cag Gln	atc Ile	ctg Leu	agc Ser 500	cgc Arg	tac Tyr	gac Asp	atc Ile 505	gcc Ala	ctg Leu	gtc Val	cag Gln	gag Glu 510	gtc Val	aga Arg	gac Asp	1536

agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac	1584
Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp	
515 520 525	
gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac	1632
Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn	
530 535 540	
agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct	1680
Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser	
545 550 555 560	
gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac	1728
Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn	
565 570 575	
gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc	1776
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe	
580 585 590	
aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg	1824
Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly	
595 600 605	
gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc	1872
Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val	
610 615 620	
caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat	1920
Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn	
625 630 635 640	
gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg	1968
Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu	
645 650 655	
tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc	2016
Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr	
660 665 670	
aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg	2064
Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly	
675 680 685	
atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac	2112
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn	
690 695 700	
ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt	2160
Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser	
705 710 715 720	
gac cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag	2208
Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys	
725 730 735	
aag cgc aag gtt tga	2223
Lys Arg Lys Val	

740

&lt;210&gt; 58

&lt;211&gt; 740

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 58

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430  
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445  
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460  
 Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
 465 470 475 480  
 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
 485 490 495  
 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
 500 505 510  
 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
 515 520 525  
 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
 530 535 540  
 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
 545 550 555 560  
 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
 565 570 575  
 Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
 580 585 590  
 Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
 595 600 605  
 Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
 610 615 620  
 Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
 625 630 635 640

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
645 650 655

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
660 665 670

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
675 680 685

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
690 695 700

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
705 710 715 720

Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys  
725 730 735

Lys Arg Lys Val  
740

<210> 59

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 59

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
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aagggcccat	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacgggtgtc	gtggaactca	540
ggcgccctga	ccagcggcgt	gcacaccttc	cgggctgtcc	tacagtcctc	aggactctac	600
tccctcagca	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgccc	accgtgccc	gcacctgaac	tcctgggggg	accgtcagtc	780
ttcctcttcc	ccccaaaacc	caaggacacc	ctcatgatct	cccggacccc	tgaggtcaca	840
tgctgtgggtg	tggacgtgag	ccacgaagac	cctgagggtca	agttcaactg	gtacgtggac	900
ggcgtggagg	tgcataatgc	caagacaaag	ccgcgggagg	agcagtacaa	cagcacgtac	960
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ccctttaact	tccaggctgc	ctatggcctg	agtgaccaac	tggccaagc	catcagtgc	2160
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<210> 60

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2220)

<223>

<400> 60

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1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 245 250 255	768
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270	816
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 275 280 285	864
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300	912
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430	1296
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
ccg ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 465 470 475 480	1440
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 485 490 495	1488
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser 500 505 510	1536
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala 515 520 525	1584
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac agc Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser 530 535 540	1632
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala 545 550 555 560	1680
gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp 565 570 575	1728
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr 580 585 590	1776
gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp 600 605 610	1824

595					600					605						
gca	gta	gcc	gag	atc	gac	gct	ctc	tat	gac	gtc	tac	ctg	gat	gtc	caa	1872
Ala	Val	Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	
610					615					620						
gag	aaa	tgg	ggc	ttg	gag	gac	gtc	atg	ttg	atg	ggc	gac	ttc	aat	gcg	1920
Glu	Lys	Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	
625					630					635					640	
ggc	tgc	agc	tat	gtg	aga	ccc	tcc	cag	tgg	tca	tcc	atc	cgc	ctg	tgg	1968
Gly	Cys	Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	
645					650					655						
aca	agc	ccc	acc	ttc	cag	tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	aca	2016
Thr	Ser	Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	
660					665					670						
gct	aca	ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	atg	2064
Ala	Thr	Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	
675					680					685						
ctg	ctc	cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	aac	ttc	2112
Leu	Leu	Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn	Phe	
690					695					700						
cag	gct	gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac	2160
Gln	Ala	Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp	
705					710					715					720	
cac	tat	cca	gtg	gag	gtg	atg	ctg	aag	ggg	ggc	gga	ccc	aaa	aag	aag	2208
His	Tyr	Pro	Val	Glu	Val	Met	Leu	Lys	Gly	Gly	Gly	Pro	Lys	Lys	Lys	
725					730					735						
cgc	aag	gtt	tga													2220
Arg	Lys	Val														

&lt;210&gt; 61

&lt;211&gt; 739

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 61

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80  
 Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110  
 Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125  
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140  
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160  
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175  
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190  
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205  
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220  
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
                   260                                  265                                  270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
                   275                                  280                                  285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
           290                                  295                                  300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
   305                                  310                                  315                                  320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
                                   325                                  330                                  335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
                   340                                  345                                  350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
           355                                  360                                  365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
       370                                  375                                  380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
   385                                  390                                  395                                  400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
                   405                                  410                                  415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
                   420                                  425                                  430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
           435                                  440                                  445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
       450                                  455                                  460

Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
   465                                  470                                  475                                  480

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
                   485                                  490                                  495

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
500 505 510

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
515 520 525

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
530 535 540

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
545 550 555 560

Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
565 570 575

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
580 585 590

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
595 600 605

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
610 615 620

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
625 630 635 640

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
645 650 655

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
660 665 670

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
675 680 685

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
690 695 700

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
705 710 715 720

His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys

725

730

735

Arg Lys Val

&lt;210&gt; 62

&lt;211&gt; 1548

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 62

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcttggt ttgcttactg gggccaaggg actctgggtc cagtctcttc agcctccacc	420
aagggcccat cggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggaactcttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccc gcacctgaag gcgggctgaa gatcgcagcc	780
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	840
gtgcagatcc tgagccgcta cgacatcgcc ctgggtccagg aggtcagaga cagccacctg	900
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcactac	960
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg	1020
cctgaccagg tgtctgcggg ggacagctac tactacgatg atggctgcga gccctgcggg	1080
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgggt cacagaggtc	1140



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agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 1200
gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgatcatgttg 1260
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cccacgcact gtgcctatga caggatcggtg gttgcaggga tgctgctccg aggggcccgtt 1440
gttcccgcact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg 1500
gccaagcca tcagtacca ctatccagtg gaggtgatgc tgaagtga 1548

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<210> 63

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 63

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca 180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240
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gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
tttgcttggg ttgcttactg gggccaaggg actctgggtc cagtctcttc agcctccacc 420
aagggcccat cggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
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gacaaaactc acacatgtcc accgtgtcca gcaccagagg gcgggctgaa gatcgagcc 780
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 840

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gtgcagatcc tgagccgcta cgacatcgcc ctggtccagg aggtcagaga cagccacctg      900
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcactac      960
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg     1020
cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg     1080
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgggt cacagaggtc     1140
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gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgtcatgttg     1260
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cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggggccggt     1440
gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg     1500
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<210> 64

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 64

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aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc     180
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agatacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc caciaacaca     300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga     360
tcctacgact ttgcctgggt tgettactgg ggccaaggga ctctggtcac agtctcctca     420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg     480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtc     540
tggaactcag gcgcctgac cagcggcgtg cacaccttcc cggctgtcct acagtctca     600

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aaatcttgtg acaaaaactca cacatgtcca ccgtgtccag caccagaggg cgggctgaag 780
atcgcagcct tcaacatcca gacatttggg gagaccaaga tgtccaatgc caccctcgtc 840
agctacattg tgcagatcct gagccgctac gacatcgccc tggccagga ggtcagagac 900
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gagatcgacg ctctctatga cgtctacctg gatgtccaag agaaatgggg cttggaggac 1260
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acagctacac ccacgcactg tgcctatgac aggatcgtag ttgcagggat gctgctccga 1440
ggggccggtg ttcccgactc ggctcttccc tttaacttcc aggctgccta tggcctgagt 1500
gaccaactgg cccaagccat cagtgaccac tatccagtgg aggtgatgct gaagtga 1557

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<210> 65

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1548)

<223>

<400> 65

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15	48
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	96
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60	192
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80	240
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95	288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125	384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggc ggg ctg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu 245 250 255	768
aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag atg tcc Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser 260 265 270	816
aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc tac gac Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp 275 280 285	864
atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc gtg ggg Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly 290 295 300	912
aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat cac tac Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr 305 310 315 320	960
gtg gtc agt gag cca ctg gga cgg aac agc tat aag gag cgc tac ctg Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu 325 330 335	1008
ttc gtg tac agg cct gac cag gtg tct gcg gtg gac agc tac tac tac Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr 340 345 350	1056
gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga gag cca Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro 355 360 365	1104
gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc agg gag ttt gcc Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala 370 375 380	1152
att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag atc gac Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp 385 390 395 400	1200
gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc ttg gag Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu 405 410 415	1248
gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat gtg aga Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg 420 425 430	1296
ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc ttc cag Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln 435 440 445	1344
tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg cac tgt Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys 450 455 460	1392
gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg gcc gtt Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val	1440

465	470	475	480	
gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat ggc ctg				1488
Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu				
	485	490	495	
agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg gag gtg				1536
Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val				
	500	505	510	
atg ctg aag tga				1548
Met Leu Lys				
	515			

&lt;210&gt; 66

&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 66

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu  
 245 250 255

Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser  
 260 265 270

Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp  
 275 280 285

Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly  
 290 295 300

Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr  
 305 310 315 320

Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu  
 325 330 335

Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr  
 340 345 350

Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro  
 355 360 365

Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala  
 370 375 380

Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp  
 385 390 395 400

Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu  
 405 410 415

Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg  
 420 425 430

Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln  
 435 440 445

Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys  
 450 455 460

Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val  
 465 470 475 480

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu  
 485 490 495

Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val  
 500 505 510

Met Leu Lys  
 515

<210> 67

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion



<400> 67  
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca 180  
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240  
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
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aagggcccat cgggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 480  
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tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 660  
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gtcagagaca gccacctgac tgccgtgggg aagctgctgg acaacctcaa tcaggacgca 960  
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ggcctgagtg accaactggc ccaagccatc agtgaccact atccagtgga ggtgatgctg 1560  
aagtga 1566

<210> 68

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 68

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggtcca	180
ggaaagggcc tgcagtggtt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctgg ttgcttactg gggccaaggg actctgggtc cagtctcttc agcctccacc	420
aaggggcccat cgggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcttc aggactctac	600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga ggggagcggc	780
gggctgaaga tcgcagcctt caacatccag acatctgggg agaccaagat gtccaatgcc	840
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cagtggtcat ccatccgcct gtggacaagc cccaccttcc agtggctgat ccccgacagc	1380

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 ggctgagtg accaactggc ccaagccatc agtgaccact atccagtgga ggtgatgctg 1560  
 aagtga 1566

<210> 69

<211> 1575

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 69

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 aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc 180  
 caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct 240  
 agatacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacaca 300  
 gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga 360  
 tcctacgact ttgcctgggt tgcttactgg ggccaaggga ctctggtcac agtctcctca 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtc 540  
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 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg aaaaaactca cacatgctgt gtcgagtgtc caccgtgtcc agcaccagag 780  
 gggagcggcg ggctgaagat cgcagccttc aacatccaga catttgggga gaccaagatg 840  
 tccaatgcca ccctcgtcag ctacattgtg cagatcctga gccgctacga catcgccctg 900  
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 caggacgcac cagacaccta tcactacgtg gtcagtgagc cactgggacg gaacagctat 1020  
 aaggagcgt acctgttcgt gtacaggcct gaccaggtgt ctgcggtgga cagctactac 1080

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gctgcctatg gcctgagtga ccaactggcc caagccatca gtgaccacta tccagtggag 1560
gtgatgctga agtga 1575

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<210> 70

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1566)

<223>

<400> 70

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1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

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gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95			288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110			336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125			384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140			432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160			480
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tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190			576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205			624
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gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro 245 250 255			768
gaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 260 265 270			816
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 275 280 285			864
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc			912

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cca Pro 325	gac Asp 325	acc Thr 325	tat Tyr 325	cac His 325	tac Tyr 325	gtg Val 325	gtc Val 325	agt Ser 330	gag Glu 330	cca Pro 330	ctg Leu 330	gga Gly 335	cgg Arg 335	aac Asn 335	agc Ser 335	1008
tat Tyr 340	aag Lys 340	gag Glu 340	cgc Arg 340	tac Tyr 340	ctg Leu 340	ttc Phe 345	gtg Val 345	tac Tyr 345	agg Arg 345	cct Pro 350	gac Asp 350	cag Gln 350	gtg Val 350	tct Ser 350	gcg Ala 350	1056
gtg Val 355	gac Asp 355	agc Ser 355	tac Tyr 355	tac Tyr 355	tac Tyr 355	gat Asp 360	gat Asp 360	ggc Gly 360	tgc Cys 360	gag Glu 365	ccc Pro 365	tgc Cys 365	ggg Gly 365	aac Asn 365	gac Asp 365	1104
acc Thr 370	ttc Phe 370	aac Asn 370	cga Arg 375	gag Glu 375	cca Pro 375	gcc Ala 375	att Ile 375	gtc Val 380	agg Arg 380	ttc Phe 380	ttc Phe 380	tcc Ser 385	cgg Arg 385	ttc Phe 385	aca Thr 385	1152
gag Glu 385	gtc Val 385	agg Arg 390	gag Glu 390	ttt Phe 390	gcc Ala 390	att Ile 390	gtt Val 395	ccc Pro 395	ctg Leu 395	cat His 395	gcg Ala 400	gcc Ala 400	ccg Pro 400	ggg Gly 400	gac Asp 400	1200
gca Ala 405	gta Val 405	gcc Ala 405	gag Glu 405	atc Ile 405	gac Asp 410	gct Ala 410	ctc Leu 410	tat Tyr 410	gac Asp 410	gtc Val 415	tac Tyr 415	ctg Leu 415	gat Asp 415	gtc Val 415	caa Gln 415	1248
gag Glu 420	aaa Lys 420	tgg Trp 420	ggc Gly 420	ttg Leu 425	gag Glu 425	gac Asp 425	gtc Val 425	atg Met 425	ttg Leu 430	atg Met 430	ggc Gly 430	gac Asp 430	ttc Phe 430	aat Asn 435	gcg Ala 435	1296
ggc Gly 435	tgc Cys 435	agc Ser 435	tat Tyr 435	gtg Val 440	aga Arg 440	ccc Pro 440	tcc Ser 440	cag Gln 445	tgg Trp 445	tca Ser 445	tcc Ser 445	atc Ile 445	cgc Arg 445	ctg Leu 450	tgg Trp 450	1344
aca Thr 450	agc Ser 450	ccc Pro 450	acc Thr 455	ttc Phe 455	cag Gln 455	tgg Trp 455	ctg Leu 460	atc Ile 460	ccc Pro 460	gac Asp 460	agc Ser 460	gct Ala 465	gac Asp 465	acc Thr 465	aca Thr 465	1392
gct Ala 465	aca Thr 465	ccc Pro 470	acg Thr 470	cac His 470	tgt Cys 470	gcc Ala 475	tat Tyr 475	gac Asp 475	agg Arg 475	atc Ile 475	gtg Val 480	gtt Val 480	gca Ala 480	ggg Gly 480	atg Met 480	1440
ctg Leu 485	ctc Leu 485	cga Arg 485	ggg Gly 485	gcc Ala 485	gtt Val 485	gtt Val 490	ccc Pro 490	gac Asp 490	tcg Ser 490	gct Ala 495	ctt Leu 495	ccc Pro 495	ttt Phe 495	aac Asn 495	ttc Phe 495	1488
cag Gln 500	gct Ala 500	gcc Ala 500	tat Tyr 500	ggc Gly 505	ctg Leu 505	agt Ser 505	gac Asp 505	caa Gln 505	ctg Leu 510	gcc Ala 510	caa Gln 510	gcc Ala 510	atc Ile 510	agt Ser 510	gac Asp 510	1536
cac His 515	tat Tyr 515	cca Pro 515	gtg Val 520	gag Glu 520	gtg Val 520	atg Met 520	ctg Leu 520	aag Lys 520	tga							1566

&lt;210&gt; 71

&lt;211&gt; 521

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 71

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
	50					55					60				

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65					70					75					80

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
				85					90					95	

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105						110	

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
		115					120					125			

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	130					135					140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150					155					160

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
				165					170					175	

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190  
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205  
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220  
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240  
 Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255  
 Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 260 265 270  
 Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 275 280 285  
 Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 290 295 300  
 His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 305 310 315 320  
 Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 325 330 335  
 Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 340 345 350  
 Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 355 360 365  
 Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 370 375 380  
 Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 385 390 395 400  
 Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln



	405		410		415
Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala	420	425		430	
Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp	435	440		445	
Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr	450	455		460	
Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met	465	470	475		480
Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe	485	490		495	
Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp	500	505		510	
His Tyr Pro Val Glu Val Met Leu Lys	515	520			

&lt;210&gt; 72

&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 72

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccag	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctggt ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420

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aagggcccat cggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg      480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca      540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc      660
aacgtgaatc acaagccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      720
gacaaaactc acacatgctg tgtggagtgc ccaccgtgcc cagcacctga aggcgggctg      780
aagatcgtag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccacctc      840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctgggtcca ggaggtcaga      900
gacagccacc tgactgccgt ggggaagctg ctggacaacc tcaatcagga cgcaccagac      960
acctatcact acgtgggtcag tgagccactg ggacggaaca gctataagga gcgctacctg     1020
ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tgatggctgc     1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcaggtt cttctcccgg     1140
ttcacagagg tcagggagtt tgccattggt cccctgcatg cggccccggg ggacgcagta     1200
gccgagatcg acgtctctta tgacgtctac ctggatgtcc aagagaaatg gggcttgagg     1260
gacgtcatgt tgatgggca cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg     1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgtgac     1380
accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc     1440
cgagggggccg ttgttccga ctcggtctt ccttttaact tccaggctgc ctatggcctg     1500
agtgaccaac tggccaagc catcagtgc cactatccag tggaggtgat gctgaagtga     1560

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<210> 73

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 73

```

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccag      60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg ggcctcagt gaaggtgtcc     120

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```

tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
tttgccctgg ttgcttactg gggccaaggg actctgggtc cagtctcctc agcctccacc 420
aaggggcccat cggctcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtctc aggactctac 600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga gggcgggctg 780
aagatcgag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc 840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctgggtcca ggaggtcaga 900
gacagccacc tgactgccgt ggggaagctg ctggacaacc tcaatcagga cgcaccagac 960
acctatcact acgtgggtcag tgagccactg ggacggaaca gctataagga gcgctacctg 1020
ttcgtgtaca ggctgacca ggtgtctgcg gtggacagct actactacga tgatgggtgc 1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcaggtt cttctcccgg 1140
ttcacagagg tcagggagtt tgccattgtt cccctgcatg cggccccggg ggacgcagta 1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttgag 1260
gacgtcatgt tgatgggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg 1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgtgac 1380
accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc 1440
cgagggggccg ttgttcccga ctcggtctt cctttaaact tccaggctgc ctatggcctg 1500
agtgaccaac tggccaagc catcagtgac cactatccag tggaggtgat gctgaagtga 1560

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<210> 74

<211> 1569

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 74

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gccgccacca tgggatggag ctgtatcatc ctcttcttgg tagcaacagc tacaggtgtc      60
cactcccagg tgcagctggg gcagctctggg gcagaggtga aaaagcctgg ggcctcagtg      120
aaggtgtcct gcaaggcttc tggctacacc ttcagtgctt actggataga gtgggtgcgc      180
caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct      240
agatacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaaacaca      300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga      360
tcctacgact ttgcctgggt tgccttactgg ggccaaggga ctctgggtcac agtctcctca      420
gcctccacca agggcccac cgtcttcccc ctggcaccct cctccaagag cacctctggg      480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg      540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtctca      600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      720
aaatcttgtg aaaaaactca cacatgctgt gtcgagtgtc caccgtgtcc agcaccagag      780
ggcgggctga agatcgcagc cttcaacatc cagacatttg gggagaccaa gatgtccaat      840
gccaccctcg tcagctacat tgtgcagatc ctgagccgct acgacatcg cctgggtccag      900
gaggtcagag acagccacct gactgccgtg gggaagctgc tggacaacct caatcaggac      960
gcaccagaca cctatcacta cgtgggtcagt gagccactgg gacggaacag ctataaggag     1020
cgctacctgt tcgtgtacag gcctgaccag gtgtctgcgg tggacagcta ctactacgat     1080
gatggctgcg agccctgcgg gaacgacacc ttcaaccgag agccagccat tgtcaggttc     1140
ttctcccggg tcacagaggt cagggagttt gccattgttc ccctgcatgc ggccccgggg     1200
gacgcagtag ccgagatcga cgtctcttat gacgtctacc tggatgtcca agagaaatgg     1260
ggcttggagg acgtcatggt gatgggagac ttcaatgcgg gctgcagcta tgtgagaccc     1320
tcccagtggt catccatccg cctgtggaca agccccacct tccagtggct gatccccgac     1380
agcgtgaca ccacagctac acccacgcac tgtgcctatg acaggatcgt ggttgcaggg     1440
atgctgctcc gaggggccgt tgttcccagc tcggctcttc cttttaactt ccaggctgcc     1500
tatggcctga gtgaccaact ggcccaagcc atcagtgacc actatccagt ggaggtgatg     1560
ctgaagtga                                     1569

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&lt;210&gt; 75

&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1560)

&lt;223&gt;

&lt;400&gt; 75

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn	
65 70 75 80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	432

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
130						135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct	768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
				245					250					255		
gaa	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	ggg	gag	816
Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	
			260					265					270			
acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	atc	ctg	864
Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	
		275					280					285				
agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	cac	ctg	912
Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	
	290					295				300						
act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	cca	gac	960
Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	
305					310					315					320	
acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cgg	aac	agc	tat	aag	1008
Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	
				325					330					335		
gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac	1056
Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	
			340					345					350			
agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	ttc	1104
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	
		355					360					365				

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aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc      1152
Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
    370                      375                      380

agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta      1200
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val
    385                      390                      395                      400

gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa      1248
Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys
                405                      410                      415

tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc      1296
Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys
                420                      425                      430

agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc      1344
Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser
                435                      440                      445

ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca      1392
Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr
                450                      455                      460

ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc      1440
Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu
    465                      470                      475                      480

cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct      1488
Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala
                485                      490                      495

gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat      1536
Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr
                500                      505                      510

cca gtg gag gtg atg ctg aag tga      1560
Pro Val Glu Val Met Leu Lys
    515

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<210> 76

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 76

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1          5          10          15

```

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80  
 Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110  
 Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125  
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140  
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160  
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175  
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190  
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205  
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220  
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240  
 Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro



				245						250						255
Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu	
			260					265					270			
Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu	
		275					280					285				
Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu	
	290					295					300					
Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp	
305					310					315					320	
Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys	
				325					330					335		
Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp	
			340					345					350			
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe	
		355					360					365				
Asn	Arg	Glu	Pro	Ala	Ile	Val	Arg	Phe	Phe	Ser	Arg	Phe	Thr	Glu	Val	
	370					375					380					
Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val	
385					390					395					400	
Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys	
				405					410					415		
Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	Gly	Cys	
			420					425					430			
Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	Thr	Ser	
		435					440					445				
Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr	
	450					455					460					
Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	Leu	Leu	
465					470					475					480	

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala  
485 490 495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
500 505 510

Pro Val Glu Val Met Leu Lys  
515

<210> 77

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 77

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gtgcagctgg	tgcagtctgg	ggcagaggtg	aaaaagcctg	gggcctcagt	gaaggtgtcc	120
tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagatacaat	240
gagaagttca	agggccgagt	gacagtcact	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgcttgg	ttgcttactg	gggccaaagg	actctggtca	cagtctcctc	agcctccacc	420
aagggcccat	cggctcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctgggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacgggtgtc	gtggaactca	540
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	aggactctac	600
tcctctcagca	gcgtggtgac	cgtgccctcc	agcagcttgg	gcaccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgctg	tgtggagtg	ccaccgtgcc	cagcacctga	aggcaggctg	780
aagatcgag	ccttcaacat	ccagacat	ggggagacca	agatgtccaa	tgccaccctc	840
gtcagctaca	ttgtgcagat	cctgagccgc	tacgacatcg	ccctgggtcca	ggaggtcaga	900
gacagccacc	tgactgccgt	ggagaagctg	ctggacaacc	tcaatcagga	cgcaccagac	960

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acctatcact acgtgggtcag tgagccactg ggacggaaca gctataagga gcgctacctg 1020
ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tgatggctgc 1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccgg 1140
ttcacagagg tcagggagtt tgccattggt cccctgcatg cggccccggg ggacgcagta 1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttgagg 1260
gacgtcatgt tgatgggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg 1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgctgac 1380
accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc 1440
cgagggggccg ttgttcccga ctcggtctt cctttaact tccaggctgc ctatggcctg 1500
agtgaccaac tggcccaagc catcagtgc cactatccag tggaggtgat gctgaagtga 1560

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<210> 78

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 78

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atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacagggtg ccactcccag 60
gtgcagctgg tgcagtctgg ggcagagggtg aaaaagcctg ggcctcagt gaagggtgtcc 120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca 180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat 240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
tttgcttggg ttgcttactg gggccaaggg actctgggtc agtctctctc agcctccacc 420
aagggcccat cggctctccc cctggcacc cctccaaga gcacctctgg gggcacagcg 480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtctc aggactctac 600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720

```

```

gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga gggcaggctg      780
aagatcgcag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc      840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctgggtcca ggaggtcaga      900
gacagccacc tgactgccgt ggagaagctg ctggacaacc tcaatcagga cgcaccagac      960
acctatcact acgtgggtcag tgagccactg ggacggaaca gctataagga gcgctacctg     1020
ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tgatggctgc     1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccgg     1140
ttcacagagg tcagggagtt tgccattggt cccctgcatg cggccccggg ggacgcagta     1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttgagg     1260
gacgtcatgt tgatggggca cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg     1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgctgac     1380
accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc     1440
cgagggggccg ttgttccga ctcggctctt ccctttaact tccaggctgc ctatggcctg     1500
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<210> 79

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1560)

<223>

<400> 79

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt      48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

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gtc	cac	tcc	cag	gtg	cag	ctg	gtg	cag	tct	ggg	gca	gag	gtg	aaa	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			
cct	ggg	gcc	tca	gtg	aag	gtg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					
gag	tgg	gtc	gga	gag	att	tta	cct	gga	agt	aat	aat	tct	aga	tac	aat	240
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70				75						80	
gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
				85					90					95		
aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			
tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				
caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165				170					175			
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
			180					185					190			
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
		210				215					220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct	768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
				245					250					255		

gaa ggc agg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag	816
Glu Gly Arg Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu	
260 265 270	
acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg	864
Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu	
275 280 285	
agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg	912
Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu	
290 295 300	
act gcc gtg gag aag ctg ctg gac aac ctc aat cag gac gca cca gac	960
Thr Ala Val Glu Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp	
305 310 315 320	
acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac agc tat aag	1008
Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys	
325 330 335	
gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac	1056
Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp	
340 345 350	
agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc	1104
Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe	
355 360 365	
aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc	1152
Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val	
370 375 380	
agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta	1200
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val	
385 390 395 400	
gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa	1248
Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys	
405 410 415	
tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc	1296
Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys	
420 425 430	
agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc	1344
Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser	
435 440 445	
ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca	1392
Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr	
450 455 460	
ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc	1440
Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu	
465 470 475 480	
cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct	1488
Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala	

	485		490		495	
gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat						1536
Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr						
	500		505		510	
cca gtg gag gtg atg ctg aag tga						1560
Pro Val Glu Val Met Leu Lys						
	515					

&lt;210&gt; 80

&lt;211&gt; 519

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 80

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255

Glu Gly Arg Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu  
 260 265 270

Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu  
 275 280 285

Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu  
 290 295 300

Thr Ala Val Glu Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp  
 305 310 315 320

Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys  
 325 330 335

Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp  
 340 345 350

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe  
 355 360 365



Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val  
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys  
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys  
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser  
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr  
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu  
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala  
 485 490 495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
 500 505 510

Pro Val Glu Val Met Leu Lys  
 515

<210> 81

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 81

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gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg ggcctcagt gaaggtgtcc 120

tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagatacaat	240
gagaagttca	agggccgagt	gacagtcact	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgcttgg	ttgcttactg	gggccaaggg	actctgggtc	cagtctcttc	agcctccacc	420
aagggcccat	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacgggtgtc	gtggaactca	540
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcttc	aggactctac	600
tccctcagca	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgccc	accgtgccc	gcacctgaag	gcgggctgaa	gatcgcagcc	780
ttcaacatcc	agacatttgg	ggagaccaag	atgtccaatg	ccaccctcgt	cagctacatt	840
gtgcagatcc	tgagccgcta	cgacatcgcc	ctgggtccagg	aggtcagaga	cagccacctg	900
actgccgtgg	ggaagctgct	ggacaacctc	aatcaggacg	caccagacac	ctatcactac	960
gtggtcagt	agccactggg	acggaacagc	tataaggagc	gctacctgtt	cgtgtacagg	1020
cctgaccagg	tgtctgcggt	ggacagctac	tactacgatg	atggctgcga	gccctgcggg	1080
aacgacacct	tcaaccgaga	gccagccatt	gtcaggttct	tctcccgggt	cacagaggtc	1140
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gctctctatg	acgtctacct	ggatgtccaa	gagaaatggg	gcttgaggga	cgtcatgttg	1260
atgggcgact	tcaatgcggg	ctgcagctat	gtgagaccct	cccagtggtc	atccatccgc	1320
ctgtggacaa	gccccacctt	ccagtggctg	atccccgaca	gcgctgacac	cacagctaca	1380
cccacgcact	gtgcctatga	caggatcggt	gttgaggga	tgctgctccg	aggggcccgtt	1440
gttcccgaact	cggtctcttc	ctttaacttc	caggctgcct	atggcctgag	tgaccaactg	1500
gccaagcca	tcagtgacca	ctatccagt	gaggtgatgc	tgaagggggg	cggacccaaa	1560
aagaagcgca	aggtttga					1578

&lt;210&gt; 82

&lt;211&gt; 1578

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 82

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gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
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ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
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aagaagcgca aggtttga 1578

<210> 83

<211> 1587

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 83

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caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct 240  
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<210> 84

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1578)

<223>

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<400> 84
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gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn

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65	70					75					80					
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac	Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn					85 90 95										288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc	Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val					100 105 110										336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc	Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly					115 120 125										384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg	Gln Gly Thr Leu Val Thr Ser Ser Ala Ser Thr Lys Gly Pro Ser					130 135 140										432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala					145 150 155 160										480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val					165 170 175										528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala					180 185 190										576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val					195 200 205										624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac	Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His					210 215 220										672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt	Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys					225 230 235 240										720
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggc ggg ctg	Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu					245 250 255										768
aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag atg tcc	Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser					260 265 270										816
aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc tac gac	Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp					275 280 285										864
atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc gtg ggg	Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly					290 295 300										912
aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat cac tac																960

Lys 305	Leu	Leu	Asp	Asn	Leu 310	Asn	Gln	Asp	Ala	Pro 315	Asp	Thr	Tyr	His	Tyr 320	
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Val	Val	Ser	Glu	Pro 325	Leu	Gly	Arg	Asn	Ser 330	Tyr	Lys	Glu	Arg	Tyr 335	Leu	
ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac	agc	tac	tac	tac	1056
Phe	Val	Tyr	Arg 340	Pro	Asp	Gln	Val	Ser 345	Ala	Val	Asp	Ser	Tyr 350	Tyr	Tyr	
gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	ttc	aac	cga	gag	cca	1104
Asp	Asp	Gly 355	Cys	Glu	Pro	Cys	Gly 360	Asn	Asp	Thr	Phe	Asn 365	Arg	Glu	Pro	
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Ala	Ile 370	Val	Arg	Phe	Phe	Ser 375	Arg	Phe	Thr	Glu	Val 380	Arg	Glu	Phe	Ala	
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Ile	Val	Pro	Leu	His 385	Ala	Ala 390	Pro	Gly	Asp 395	Ala	Val	Ala	Glu	Ile	Asp 400	
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Ala	Leu	Tyr	Asp 405	Val	Tyr	Leu	Asp	Val 410	Gln	Glu	Lys	Trp	Gly	Leu 415	Glu	
gac	gtc	atg	ttg	atg	ggc	gac	ttc	aat	gcg	ggc	tgc	agc	tat	gtg	aga	1296
Asp	Val	Met	Leu 420	Met	Gly	Asp	Phe	Asn 425	Ala	Gly	Cys	Ser	Tyr 430	Val	Arg	
ccc	tcc	cag	tgg	tca	tcc	atc	cgc	ctg	tgg	aca	agc	ccc	acc	ttc	cag	1344
Pro	Ser	Gln 435	Trp	Ser	Ser	Ile	Arg 440	Leu	Trp	Thr	Ser	Pro 445	Thr	Phe	Gln	
tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	aca	gct	aca	ccc	acg	cac	tgt	1392
Trp	Leu	Ile	Pro	Asp	Ser	Ala 455	Asp	Thr	Thr	Ala	Thr 460	Pro	Thr	His	Cys	
gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	atg	ctg	ctc	cga	ggg	gcc	gtt	1440
Ala	Tyr	Asp	Arg	Ile	Val 465	Val 470	Ala	Gly	Met 475	Leu	Leu	Arg	Gly	Ala 480	Val	
gtt	ccc	gac	tgc	gct	ctt	ccc	ttt	aac	ttc	cag	gct	gcc	tat	ggc	ctg	1488
Val	Pro	Asp	Ser 485	Ala	Leu	Pro	Phe	Asn 490	Phe	Gln	Ala	Ala	Tyr	Gly 495	Leu	
agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac	cac	tat	cca	gtg	gag	gtg	1536
Ser	Asp	Gln	Leu 500	Ala	Gln	Ala	Ile	Ser 505	Asp	His	Tyr	Pro 510	Val	Glu	Val	
atg	ctg	aag	ggg	ggc	gga	ccc	aaa	aag	aag	cgc	aag	gtt	tga			1578
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<211> 525

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 85

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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala



[illegible]

Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg  
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Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln  
                   435                  440                  445

Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys  
                   450                  455                  460

Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val  
                   465                  470                  475                  480

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu  
                   485                  490                  495

Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val  
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Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys Val  
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<210> 86

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd -DNase I fusion

<400> 86

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
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gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcttggt ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc	420
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ggcctgagtg accaactggc ccaagccatc agtgaccact atccagtgga ggtgatgctg 1560
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<210> 87

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 87

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca 180

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gagctcagca gcctgagggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360
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aaggggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480
gccctggggt gcttgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
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<210> 88

<211> 1605

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 88

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1605

<210> 89

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1596)

<223>

<400> 89

atg	gga	tgg	agc	tgt	atc	atc	ctc	ttc	ttg	gta	gca	aca	gct	aca	ggt	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1				5					10					15		

gtc	cac	tcc	cag	gtg	cag	ctg	gtg	cag	tct	ggg	gca	gag	gtg	aaa	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			

cct	ggg	gcc	tca	gtg	aag	gtg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				

agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					

gag	tgg	gtc	gga	gag	att	tta	cct	gga	agt	aat	aat	tct	aga	tac	aat	240
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70				75						80	

gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
			85					90						95		

aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			

tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro 245 250 255	768
gaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 260 265 270	816
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 275 280 285	864
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser 290 295 300	912
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala 305 310 315 320	960
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac agc Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser 325 330 335	1008
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala 340 345 350	1056
gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp	1104

355	360	365	
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca			1152
Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr			
370	375	380	
gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac			1200
Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp			
385	390	395	400
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa			1248
Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln			
	405	410	415
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg			1296
Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala			
	420	425	430
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg			1344
Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp			
	435	440	445
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca			1392
Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr			
	450	455	460
gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg			1440
Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met			
465	470	475	480
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc			1488
Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe			
	485	490	495
cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac			1536
Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp			
	500	505	510
cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag			1584
His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys			
	515	520	525
cgc aag gtt tga			1596
Arg Lys Val			
530			

&lt;210&gt; 90

&lt;211&gt; 531

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;



<223> Humanised HMFG1 Fd - DNase I fusion

<400> 90

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240  
 Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255  
 Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 260 265 270  
 Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 275 280 285  
 Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 290 295 300  
 His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 305 310 315 320  
 Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 325 330 335  
 Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 340 345 350  
 Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 355 360 365  
 Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 370 375 380  
 Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 385 390 395 400  
 Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
 405 410 415  
 Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
 420 425 430  
 Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
 435 440 445  
 Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
 450 455 460

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
465 470 475 480

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
485 490 495

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
500 505 510

His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys  
515 520 525

Arg Lys Val  
530

<210> 91

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 91

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccag	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg ggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccctgg ttgcttactg gggccaaggg actctgggtc cagtctctc agcctccacc	420
aagggcccat cggctctccc cctggcacc cctccaaga gcacctctgg gggcacagcg	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtctc aggactctac	600
tcctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660

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aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      720
gacaaaactc acacatgctg tgtggagtgc ccaccgtgcc cagcacctga aggcgggctg      780
aagatcgcag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc      840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctgggtcca ggaggtcaga      900
gacagccacc tgactgccgt ggggaagctg ctggacaacc tcaatcagga cgcaccagac      960
acctatcact acgtggctag tgagccactg ggacggaaca gctataagga gcgctacctg     1020
ttcgtgtaca ggcctgacca ggtgtctgct gtggacagct actactacga tgatggctgc     1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggt cttctcccgg     1140
ttcacagagg tcagggagtt tgccattggt ccctgcatg cggccccggg ggacgcagta     1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttgagg     1260
gacgtcatgt tgatgggcca cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg     1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgctgac     1380
accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc     1440
cgagggggccg ttgttccga ctgggtctt ccctttaact tccaggctgc ctatggcctg     1500
agtgaccaac tggccaagc catcagtgc cactatccag tggaggtgat gctgaagggg     1560
ggcggacca aaaagaagcg caaggtttga                                     1590

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<210> 92

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 92

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atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccag      60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg ggcctcagt gaaggtgtcc     120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccagggtcca     180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat     240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg     300
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac     360

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tttgcttggg ttgcttactg gggccaaggg actctgggtca cagtctcctc agcctccacc 420
aaggggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga gggcgggctg 780
aagatcgag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc 840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctgggtcca ggaggtcaga 900
gacagccacc tgactgccgt ggggaagctg ctggacaacc tcaatcagga cgcaccagac 960
acctatcact acgtgggtcag tgagccactg ggacggaaca gctataagga gcgctacctg 1020
ttcgtgtaca ggctgacca ggtgtctgcg gtggacagct actactacga tgatggctgc 1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggt cttctcccgg 1140
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gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttgag 1260
gacgtcatgt tgatgggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg 1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgtgac 1380
accacagcta caccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc 1440
cgagggggcg ttgttcccga ctcggctctt ccctttaact tccaggctgc ctatggcctg 1500
agtgaccaac tggccaagc catcagtgac cactatccag tggaggtgat gctgaagggg 1560
ggcggacca aaaagaagcg caaggtttga 1590

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<210> 93

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 93

gccgccacca tgggatggag ctgtatcatc ctcttcttgg tagcaacagc tacaggtgtc 60  
 cactcccagg tgcagctggg gcagtctggg gcagaggtga aaaagcctgg ggcctcagtg 120  
 aaggtgtcct gcaaggcttc tggctacacc ttcagtgcct actggataga gtgggtgcgc 180  
 caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct 240  
 agatacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc caciaaacaca 300  
 gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga 360  
 tcctacgact ttgcctgggt tgcttactgg ggccaaggga ctctggtcac agtctcctca 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggacacagcg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
 tggaaactcag gcgccttgac cagcggcgtg cacaccttcc cggctgtcct acagtctca 600  
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg acaaaaactca cacatgctgt gtcgagtgtc caccgtgtcc agcaccagag 780  
 ggcgggctga agatcgcagc cttcaacatc cagacatttg gggagaccaa gatgtccaat 840  
 gccaccctcg tcagctacat tgtgcagatc ctgagccgct acgacatcgc cctgggtccag 900  
 gaggtcagag acagccacct gactgccgtg gggaagctgc tggacaacct caatcaggac 960  
 gcaccagaca cctatcacta cgtgggtcagt gagccactgg gacggaacag ctataaggag 1020  
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 gatggctgcg agccctgcgg gaacgacacc ttcaaccgag agccagccat tgtcaggttc 1140  
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 gacgcagtag ccgagatcga cgctctctat gacgtctacc tggatgtcca agagaaatgg 1260  
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 tatggcctga gtgaccaact ggcccaagcc atcagtgacc actatccagt ggaggtgatg 1560  
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<210> 94

<211> 1590

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1590)

&lt;223&gt;

&lt;400&gt; 94

atg	gga	tgg	agc	tgt	atc	atc	ctc	ttc	ttg	gta	gca	aca	gct	aca	ggt	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1				5					10					15		

gtc	cac	tcc	cag	gtg	cag	ctg	gtg	cag	tct	ggg	gca	gag	gtg	aaa	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			

cct	ggg	gcc	tca	gtg	aag	gtg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				

agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					

gag	tgg	gtc	gga	gag	att	tta	cct	gga	agt	aat	aat	tct	aga	tac	aat	240
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70					75					80	

gag	aag	ttc	aag	ggc	cga	gtg	aca	gtc	act	aga	gac	aca	tcc	aca	aac	288
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
				85					90					95		

aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	agg	tct	gag	gac	aca	gcc	gtc	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105						110		

tat	tac	tgt	gca	aga	tcc	tac	gac	ttt	gcc	tgg	ttt	gct	tac	tgg	ggc	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				

caa	ggg	act	ctg	gtc	aca	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	432
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					

gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	480
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	

145	150	155	160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175				528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190				576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205				624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220				672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240				720
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro 245 250 255				768
gaa ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu 260 265 270				816
acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu 275 280 285				864
agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu 290 295 300				912
act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca cca gac Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp 305 310 315 320				960
acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac agc tat aag Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys 325 330 335				1008
gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp 340 345 350				1056
agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe 355 360 365				1104
aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val 370 375 380				1152
agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta				1200



Arg	Glu	Phe	Ala	Ile	Val	Pro	Leu	His	Ala	Ala	Pro	Gly	Asp	Ala	Val		
385					390					395					400		
gcc	gag	atc	gac	gct	ctc	tat	gac	gtc	tac	ctg	gat	gtc	caa	gag	aaa	1248	
Ala	Glu	Ile	Asp	Ala	Leu	Tyr	Asp	Val	Tyr	Leu	Asp	Val	Gln	Glu	Lys		
				405					410					415			
tgg	ggc	ttg	gag	gac	gtc	atg	ttg	atg	ggc	gac	ttc	aat	gcg	ggc	tgc	1296	
Trp	Gly	Leu	Glu	Asp	Val	Met	Leu	Met	Gly	Asp	Phe	Asn	Ala	Gly	Cys		
			420					425					430				
agc	tat	gtg	aga	ccc	tcc	cag	tgg	tca	tcc	atc	cgc	ctg	tgg	aca	agc	1344	
Ser	Tyr	Val	Arg	Pro	Ser	Gln	Trp	Ser	Ser	Ile	Arg	Leu	Trp	Thr	Ser		
		435					440					445					
ccc	acc	ttc	cag	tgg	ctg	atc	ccc	gac	agc	gct	gac	acc	aca	gct	aca	1392	
Pro	Thr	Phe	Gln	Trp	Leu	Ile	Pro	Asp	Ser	Ala	Asp	Thr	Thr	Ala	Thr		
	450					455					460						
ccc	acg	cac	tgt	gcc	tat	gac	agg	atc	gtg	gtt	gca	ggg	atg	ctg	ctc	1440	
Pro	Thr	His	Cys	Ala	Tyr	Asp	Arg	Ile	Val	Val	Ala	Gly	Met	Leu	Leu		
465					470					475					480		
cga	ggg	gcc	gtt	gtt	ccc	gac	tcg	gct	ctt	ccc	ttt	aac	ttc	cag	gct	1488	
Arg	Gly	Ala	Val	Val	Pro	Asp	Ser	Ala	Leu	Pro	Phe	Asn	Phe	Gln	Ala		
				485					490					495			
gcc	tat	ggc	ctg	agt	gac	caa	ctg	gcc	caa	gcc	atc	agt	gac	cac	tat	1536	
Ala	Tyr	Gly	Leu	Ser	Asp	Gln	Leu	Ala	Gln	Ala	Ile	Ser	Asp	His	Tyr		
			500					505					510				
cca	gtg	gag	gtg	atg	ctg	aag	ggg	ggc	gga	ccc	aaa	aag	aag	cgc	aag	1584	
Pro	Val	Glu	Val	Met	Leu	Lys	Gly	Gly	Gly	Pro	Lys	Lys	Lys	Arg	Lys		
		515					520					525					
gtt	tga															1590	
Val																	

&lt;210&gt; 95

&lt;211&gt; 529

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 95

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly		
1				5					10					15			

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					
Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn	
65					70					75					80	
Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn	
				85					90					95		
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			
Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	
		115					120					125				
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
	130					135					140					
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
145					150					155					160	
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
				165					170					175		
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
		180						185					190			
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
		195					200					205				
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	210					215					220					
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
225					230					235					240	
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
				245					250					255		

Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu  
 260 265 270  
 Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu  
 275 280 285  
 Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu  
 290 295 300  
 Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp  
 305 310 315 320  
 Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys  
 325 330 335  
 Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp  
 340 345 350  
 Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe  
 355 360 365  
 Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
 370 375 380  
 Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val  
 385 390 395 400  
 Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys  
 405 410 415  
 Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys  
 420 425 430  
 Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser  
 435 440 445  
 Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr  
 450 455 460  
 Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu  
 465 470 475 480  
 Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala

148

485

490

495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
500 505 510

Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys  
515 520 525

Val

<210> 96

<211> 7

<212> PRT

<213> Simian virus 40

<400> 96

Pro Lys Lys Lys Arg Lys Val  
1 5

<210> 97

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 97

Gly Ser Gly Gly  
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<210> 98

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Consensus ribosome binding sequence

<400> 98  
gccgccacc

9

<210> 99

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion protein

<400> 99

Pro	Asp	Thr	Arg	Pro	Pro	Asp	Thr	Arg	Pro	Pro	Asp	Thr	Arg	Pro	Pro
1				5					10					15	

Asp	Thr	Arg	Pro	Pro	Asp	Thr	Arg	Pro	Pro	Asp	Thr	Arg	Pro	Pro	Asp
			20					25					30		

Thr	Arg	Pro
		35

<210> 100

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant hinge

<400> 100

Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
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<210> 101

<211> 5

<212> PRT

<213> Homo sapiens

<400> 101

Ala Pro Asp Thr Arg  
1 5

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A35  
at